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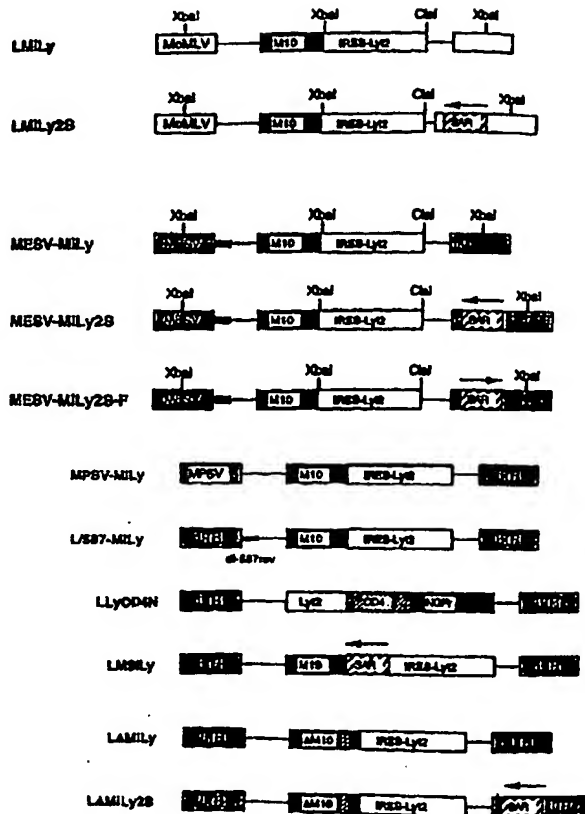
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## (54) Title: VECTORS COMPRISING SAR ELEMENTS

## (57) Abstract

Scaffold attachment regions are found to increase gene expression in transduced cells, and to be therefore useful, e.g., in gene therapy.



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### VECTORS COMPRISING SAR ELEMENTS

This invention relates to the use of scaffold attachment regions (SARs) to increase gene expression in primary non-proliferating cells i.e. in resting cells.

Eukaryotic chromosomes are organised into discrete chromatin domains which are thought to define independent units encompassing all required *cis*-regulatory elements for co-ordinated expression of the genes within the domain. These chromatin domains are bordered by sequences which specifically associate with the nuclear scaffold, or nuclear matrix, defining the boundaries of the chromatin domains. Such sequences are referred to as scaffold attachment region (SAR) or matrix attachment region (MAR). SAR elements are several hundred basepairs long and A/T rich ( $\geq 70\%$ ). Although cloned SAR and MAR elements share common structural features, no consensus sequence has been identified. SARs have been located upstream, downstream or within genes (introns) suggesting that they may represent functionally distinct classes (Bode J et al. 1995 *Scaffold/Matrix-attachment regions (S/MAR): Structural properties creating transcriptionally active loci* Academic Press, Orlando). SAR elements can enhance expression of heterologous genes in transfection experiments in vitro and in transgenic mice. In some instances, it has been reported that SAR elements can confer position-independent expression to a linked transgene.

While transfected DNA integrates randomly into chromosomes, there is growing evidence that retroviral integration is not completely random (Shih, C. C 1988 *Cell* 53, 531-537, Rohdewohld, H et al 1987 *J. Virol.* 61, 336-343 and Mielke, C et al 1996 *Biochemistry* 35, 2239-2252). Notably, proviruses preferentially integrate into host SAR sequences (Mielke, C et al 1996) and into "open" chromatin characterised by sensitivity to DNaseI digestion (Rohdewohld, H et al 1987).

Our experience has shown that the regulation of gene expression is different for resting cells as opposed to proliferating cells. We have found that gene expression of transduced genes is significantly decreased in resting (i.e. not mitotically active) cells as compared to active cells. Low expression in resting cells is a problem when expression is desired in vivo, e.g., in gene therapy, because at any given time, most cells in the body (unlike most cells in cell cultures) are in a quiescent state. Thus, although methods are now available to permit and enhance integration of heterologous genetic material into normal resting cells, there are at present no established ways to enhance expression of the heterologous genetic material in such cells.

One might suppose that the difference in expression is due to limiting quantities of necessary transcription factors or to control by specific promoter/enhancer elements. Our research suggests, however, that this difference in expression between resting and proliferating cells is largely due to changes in chromatin structure mediated by the DNA SARs. Hereinafter, use of the term SAR will be understood to encompass scaffold and matrix attachment regions.

We have now discovered that SARs increase expression of heterologous genes in transduced eukaryotic resting primary cells, particularly in retrovirally transduced cells. The SAR sequence has no detectable influence on retroviral vector expression in transduced cell lines. In contrast, the SAR-containing vectors express at significantly higher levels compared to controls in resting primary T cells. For example, we have shown that in retrovirally transduced resting primary T cells, a SAR significantly increases expression of the heterologous gene, both in terms of percentage of cells expressing that gene and in terms of levels of expression per cell. This is the first demonstration that retroviral mediated transduction of a SAR and a heterologous gene in cis improves expression of that gene, and the first demonstration that co-transduction with a SAR and a heterologous gene improves expression of the gene in resting primary cells.

Vectors suitable for use in the present invention are chosen on the basis of their ability of causing integration with the host genetic material. Accordingly, retroviruses which include oncoviruses such as Moloney C type and lentiviruses are suitable for purposes of the present invention. The invention may also be practised by introducing the DNA by homologous recombination or by using artificial human chromosomes.

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The invention thus provides, in a first embodiment

(i) Use of a SAR to increase gene expression in transduced cells for example resting cells, including resting progeny of transduced cells;

(ii) A method of increasing expression of a heterologous gene in a resting cell comprising transducing a cell, e.g., a non-immortal cell, with (i) the heterologous gene and (ii) one or more SARs.

A SAR for use in the present invention is not itself transcribed and translated to express a protein, nor is it a promoter or enhancer element for a gene; its effect on gene expression is mostly position-independent. By position-independent is understood that the SAR is placed within the vector and is not placed so as to destroy other functions required for gene transfer and expression for example the SAR should not be inserted in a position which blocks an essential LTR function. Preferably the SAR is at least 450 base pairs (bp) in length, preferably from 600-1000 bp, e.g., about 800 bp. The SAR is preferably AT-rich (i.e., more than 50%, preferably more than 70% of the bases are adenine or thymine), and will generally comprise repeated 4-6 bp motifs, e.g., ATTA, ATTTA, ATTTTA, TAAT, TAAAT, TAAAAT, TAATA, and/or ATATTT, separated by spacer sequences, e.g., 3-20 bp, usually 8-12 bp in length. The SAR may be from any eukaryote, preferably a mammal, most preferably a human. Suitably the SAR is the SAR for human IFN- $\beta$  gene or fragment thereof, e.g., preferably derived from or corresponding to the 5' SAR of human interferon beta (IFN- $\beta$ ), Klehr, D et al. Scaffold-Attached Regions from the Human Interferon  $\beta$  domain Can Be Used To Enhance the Stable Expression of Genes under the Control of Various Promoters. Biochemistry 1991, 30, 1264-1270), e.g., a fragment of at least 450 base pairs (bp) in length, preferably from 600-1000 bp, e.g., about 800 bp, and being substantially homologous to a corresponding portion of the 5' SAR of human IFN- $\beta$  gene, e.g., having at least 80%, preferably at least 90%, most preferably at least 95% homology therewith. Especially preferred for use as a SAR in accordance with the present invention is the 800 bp Eco-RI-HindIII (blunt end) fragment of the 5'SAR element of IFN- $\beta$  as described by Mielke, C et al. Biochemistry 1990 29: 7475-7485.

In a further embodiment, the invention provides:

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(i) a retroviral vector comprising genetic material corresponding to (a) at least one SAR, and (b) at least one heterologous gene operatively linked to an expression control sequence, the heterologous gene (or at least one of the heterologous genes if there is more than one heterologous gene) being rev-M10 and the SAR or at least one SAR is derived from, obtainable from or corresponds to the 5' SAR of the human interferon- $\beta$  gene;

(ii) a packaging cell line transduced with a retroviral vector according to (i) ; and

(iii) a cellular composition comprising non-immortal eukaryotic cells (preferably a mammalian, e.g., human cell) transduced with a retroviral vector according to (i). Hereinafter (i) , (ii) and (iii) above will be referred to as a retroviral vector of the invention, a packaging cell line of the invention and a cellular composition of the invention respectively.

Preferably, the retroviral vector is an amphotropic retroviral vector, preferably a vector characterized in that it has a long terminal repeat sequence (LTR), e.g., a retroviral vector derived from the Moloney murine leukemia virus (MoMLV), myeloproliferative sarcoma virus (MPSV), murine embryonic stem cell virus (MESV), murine stem cell virus (MSCV) or spleen focus forming virus(SFFV). Preferably, in the case of a vector according to (ii), the gene to be expressed replaces the retroviral *gag*, *pol* and/or *env* sequences.

Selection of an appropriate control expression sequences is dependent on the host cell used and the choice is within the skill of one of ordinary skill in the art. Examples of regulatory elements include a transcriptional promoter or enhancer or RNA polymerase binding sequence, sequences conferring inducibility of transcription, and selectable markers may be incorporated into the expression vector. The promoter controlling expression of the gene is, for example viral LTR, e.g., MoMLV LTR, tissue specific promoters, or inducible promoters. Preferably, the construct lacks the retroviral *gag*, *pol* and/or *env* sequences, so that the *gag*, *pol* and *env* functions must be provided *in trans* by a packaging cell line. Thus, when the vector construct is introduced into the packaging cell, the *gag-pol* and *env* proteins produced by the cell assemble with the vector RNA to produce replication-defective, transducing virions that are secreted into the culture medium. The virus thus produced can infect and integrate into the DNA of the target cell, but generally will not produce infectious viral particles since it is lacking essential viral sequences.

Particularly preferred vector structures comprise the general structure Type 1, Type 2 or Type 3:



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Type 1:      5'      LTR-X-SAR-m-LTR      3';  
 Type 2:      5'      LTR-X-m-SAR-LTR      3';  
 Type 3:      5'      LTR-X-m-LTR/SAR      3';

wherein LTR is a long terminal repeat, X is the gene for the desired protein, preferably the revM10 gene, m is a marker, SAR is a scaffold/matrix attachment region, preferably the hIFN $\beta$  SAR described below, and LTR/SAR is a long terminal repeat with SAR incorporated into it, for example the LMSILy (LMSiLy) or LMILy2S (LMiLy2S) vectors further described herein. Alternatively, the vector contains only the gene of interest and one or more SAR elements. In the type 3 vector structure, the SAR element is incorporated into the vector 3' LTR and thereby duplicated into the 5'LTR, resulting in a vector having two copies of the SAR element. Alternatively, two copies of the SAR are arranged to form a vector of structure (5') LTR-X-SAR-m-SAR-LTR (3'). The SAR in a single SAR system, is placed upstream of the 3' LTR. A particularly preferred system is one in which the SAR is in a single copy, in the 3' position (upstream of the 3' LTR) and in reverse orientation. The orientation of the SAR i.e. either forward or reverse is important. In order to increase expression of the heterologous gene, the SAR should be placed (in the vector) in the reverse direction. A SAR in the forward direction, down-regulates expression. This down-regulation effect is of use in a single SAR-two promoter system for example where lower expression of one gene in a multi-gene system is desired.

The packaging cell line is preferably transfected with separate plasmids encoding *gag-pol* and *env*, so that multiple recombination events are necessary before a replication-competent retrovirus (RCR) can be produced. Suitable retroviral vector packaging cell lines include those based on the murine NIH/3T3 cell line and include PA317 (Miller et al. 1986 *Mol. Cell Biol.* 6:2895; Miller et al. 1989 *BioTechniques* 7:980), CRIP (Danos et al. 1988 *Proc. Natl Acad Sci USA* 85:6460), and gp + am12 (Markowitz et al. 1988 *Virology* 167:400); and also cell lines based on human 293 cells or monkey COS cells, for example ProPak A packaging cells, e.g., as described in Pear et al. 1993 *Proc. Natl. Acad. Sci. USA* 90: 8392-8396; Rigg et al., 1996 *Virology* 218; Finer et al. 1994 *Blood* 83: 43-50; Landau, et al. 1992 *J. Virol.* 66: 5110-5113). Retroviral vector DNA can be introduced into packaging cells either by stable or transient transfection to produce retroviral vector particles.

The range of host cells that may be infected by a retrovirus or retroviral vector is generally determined by the viral *env* protein. The recombinant virus generated from a packaging cell can be used to infect virtually any cell type recognized by the *env* protein provided by the packaging cell. Infection results in the integration of the viral genome into the transduced cell and the consequent stable expression of the foreign gene product. The efficiency of infection is also related to the level of expression of the receptor on the target cell. In general, murine ecotropic *env* of MoMLV allows infection of rodent cells, whereas amphotropic *env* allows infection of rodent, avian and some primate cells, including human cells. Xenotropic vector systems utilize murine xenotropic *env*, and also allow infection of human cells. The host range of retroviral vectors may be altered by substituting the *env* protein of the base virus with that of a second virus. The resulting, "pseudotyped" virus has the host range of the virus donating the envelope protein and expressed by the packaging cell line. For example, the G-glycoprotein from vesicular stomatitis virus (VSV-G) may be substituted for the MMLV *env* protein, thereby broadening the host range. Preferably the vector and packaging cell line of the present invention are adapted to be suitable for transduction of human cells.

By heterologous gene is meant a gene which is not a native retroviral gene and which is suitably inserted into the vector under control of a promoter to permit expression in the cell to be transduced. The heterologous gene may be any gene for which expression is desired, e.g., a gene encoding for a protein which interferes with viral or retroviral (e.g., HIV) replication, for example the Rev-M10 gene, e.g., as described in WO 90/14427 and Escaich et al. Hum. Gene Ther. (1995) 6: 625-634.

The eukaryotic cells with which the method of the present invention is employed are non-immortal human cells. By "non-immortal human cell" is meant a human cell which in cell culture will grow through only a finite number of divisions, or which in vivo may undergo maturation or differentiation, e.g., a non-cancerous primary cell. Suitable cell types include cell types which undergo differentiation or activation and which become arrested in vivo, e.g., hematopoietic cells, endothelial cells, fibroblasts, keratinocytes, etc. Accordingly, the present invention encompasses the use of a SAR to increase gene expression in resting (non-proliferating) eukaryotic primary cells, the term resting including cells which were previously active and are now resting.

Preferably the cells are non-cancerous hematopoietic cells, e.g., hematopoietic stem cells (for example, CD34+ / Thy-1+ cells) or mature hematopoietic cells (e.g., peripheral blood lymphocytes or thymocytes, for example CD4+ cells).

Gene therapy is a method of therapy comprising the use of cells which express heterologous genetic material *in vivo*. In the case of treatment of an inborn genetic disease characterized by a deficiency in expression of a critical protein (e.g., ADA-deficiency (SCID), hemophilia A and B, Gaucher's disease, and the like), the genetic material is suitably a gene for the normal protein. Alternatively, the gene may be for a protective protein, e.g., a gene for a protein that protects against high dose chemotherapy, e.g., MDR-1, or a gene for a protein protecting against viral or retroviral infection, e.g., rev-M10, or may encode a protective RNA, e.g. a ribozyme or antisense sequence capable of protecting against viral or retroviral infection. Gene therapy may be *in vivo*, e.g., administering the vector to the patient, so that the target cells are transduced *in situ*, or *ex vivo*, e.g., transducing the desired cells *in vitro* and introducing the transduced cells into the patient, for example a procedure wherein the desired cells are removed and isolated from the individual to be treated, transduced with the desired gene, then reintroduced into the patient.

Peripheral blood lymphocytes (PBLs) have been used as cellular targets for gene therapy applications of immune disorders including SCID-ADA deficiency and HIV disease. At present, retroviral vectors are the gene transfer modality of choice mainly because integration of retrovirally-transduced genes into the chromosome of the target cells supports persistent transgene expression reviewed in. Protocols for efficient gene marking of PBLs have been developed, but little is known about regulation of transgene expression in primary T cells. *In vivo*, the majority of circulating PBLs are in a resting state and genes encoded by standard retroviral vectors based on the Moloney murine leukemia virus or the Murine embryonic stem cells virus are not efficiently expressed in these cells. The factors that control transgene expression in primary T cells are not known, but may render retroviral-based gene therapy approaches inefficient in certain disease applications including HIV disease.

In a yet further embodiment, the invention provides

- (i) a method of gene therapy in a patient in need thereof, comprising introducing into said patient
- a) a cellular composition of the present invention or
- b) a retroviral vector of the present invention;

(ii) a cellular composition as described above for therapeutic or prophylactic use, e.g., in a method of gene therapy as described above;

(iii) the use of a SAR or vector as described above in the manufacture of a cellular composition as described above, or in a method of gene therapy as described above.

A preferred embodiment of the present invention is a method of treating a patient suffering from HIV infection, e.g., HIV-1 infection, comprising removing and isolating hematopoietic cells (e.g., hematopoietic stem cells, peripheral blood lymphocytes, CD4+ cells or T cells derived from hematopoietic stem cells) from said patient; transducing the cells with a gene for an anti-retroviral protein (e.g., rev-M10) and a SAR (e.g., a SAR derived or obtainable from the 5' SAR of human IFN- $\beta$ ), and reintroducing the cells into the patient. Optionally, the patient may receive co-therapy with cytokines or growth factors such as IL-2, and/or with anti-HIV drugs such as AZT, HIV protease inhibitors, or the like.

Mature T-cells isolated from PBL or thymus (thymocytes) are normally in a resting state (i.e. mitotically inactive). Upon in vitro exposure to various stimuli such as phytohemagglutinin (PHA) and allogenic feeder cells or anti-CD3 and anti-CD28 antibodies the cells become activated and start to proliferate. The activation status of T-cells can be determined measuring expression of the CD25 antigen (IL-2 receptor alpha chain). CD25 expression is low on resting cells and is upregulated on activated cells. After initial activation T-cells will undergo several rounds of division and then return to non-activated state and concomitantly downregulate expression of CD25 antigen.

Figure 1 depicts schematic representations of the specific retroviral vectors described in the examples. The names of the retroviral vectors are indicated on the left. Vectors are not drawn to scale. LTR is Moloney murine leukemia virus long terminal repeat; MPSV is myeloproliferative sarcoma virus LTR; MESV is murine embryonal stem cell virus LTR; SAR is scaffold or matrix attachment region; IRES is internal ribosomal entry site; NGFr is nerve growth factor receptor.

Figure 2 depicts expression of retroviral vectors in CD25<sup>+</sup> cell populations on day 11 post stimulation.

Figure 3A is a schematic representation of the integrated LMiLy2S proviral DNA and the position of primers which are used to amplify SAR sequence present in the 5' and the 3' LTR.

Figure 3B shows the PCR analysis of the two sorted sub-populations of resting LMiLy2S-transduced T cells, Lyt-2<sup>+</sup> and Lyt-2<sup>-</sup> cells. The two populations are separated using FACS and analysed by semiquantitative PCR for the presence of the SAR sequence in the proviral DNA.

Figure 4 depicts the HIV-1 infection experiment. (A) Primary T cells are harvested on day five post-stimulation with PHA, IL-2 and feeder cells and inoculated with the HIV-1 JR-CSF virus. Viral replication is monitored over a period of 9 days by measuring p24 antigen concentration in cell supernatants. (B) "Day 5 re-stimulated" samples are re-stimulated with fresh PHA, IL-2 and feeder cells on day 3 post inoculation with HIV-1. All values are average from triplicate samples, bars indicate standard error. Where not visible, the error value is below the resolution of the graphics program.

Figure 5 depicts a comparison of the effect of SAR transduction on the steady state level of retroviral RNA in primary resting T cells and in cultured cells.

Figure 6 depicts RevM10 and Lyt-2 protein expression in LMiLy-transduced CEMSS cells. (A) RevM10 and Lyt-2 protein expression correlate. Northern blot analysis of transduced CEMSS cells. RNA from transduced, Lyt-2-enriched CEMSS cell populations is analyzed using a Rev-specific oligonucleotide probe as described (Plavec, I., et al 1997 *Gene Therapy* 7, 128-139). The transducing vectors are indicated on top.  $\Delta$ LMiLy is a control vector which does not encode the RevM10 protein (Plavec, I., et al 1997 *Gene Therapy* 7, 128-139). The genomic size transcripts are indicated by arrow. (B) CEMSS cells transduced with the indicated vectors and mock transduced control cells are stained with the anti-Lyt-2-PE antibody, fixed in 4% paraformaldehyde and then stained with the anti-Rev-FITC antibody as described (Rigg, R. J., et al 1995 *J. Immunol. Methods* 188, 187-195). The cells used for this analysis are not pre-enriched for Lyt-2 expression. The fraction of transduced cells in these populations determined by Lyt-2 staining is 30% and 26% for LMiLy and  $\Delta$ LMiLy vectors, respectively.

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Figure 7 shows the comparison between LMiLy and LMiLy2S vector expression in transduced cell lines. CEMSS (human CD4<sup>+</sup> T cell line) and PA317 (mouse fibroblast line) cells are transduced with the LMiLy and LMiLy2S vectors and Lyt-2-enriched using immunomagnetic beads. The cells are stained with anti-Lyt-2-PE antibody and analyzed by FACScan. The numbers in parenthesis display percentages of Lyt-2-positive cells.

Figure 8 shows that the LMiLy2S vector is efficiently expressed in resting T cells. Lyt-2-enriched LMiLy and LMiLy2S-transduced CD4<sup>+</sup> primary T cells are activated with PHA, IL-2 and irradiated allogenic feeder cells. On days 3 and 11 post-stimulation, cell aliquots are stained with anti-CD25 FITC and anti-Lyt-2-PE antibodies and analyzed by FACScan. Numbers indicate the percentage of Lyt-2-positive cells in the respective quadrants. Gates for background fluorescence are set based on control isotype antibodies. Mock are untransduced control cells.

Figure 6 shows that the SAR effect is orientation dependent. (A) Lyt-2-enriched CD4<sup>+</sup> primary T cells transduced with the MESV-MiLy, MESV-MiLy2S, MESV-MiLy2S-F, LMiLy and LMiLy2S vectors are stimulated with PHA, IL-2 and feeder cells. Transgene expression is analyzed on days 3, 5, 7, 10 and 12 post-stimulation as described in legend to Fig 2. On day 12, cells are re-stimulated (indicated by arrow) and analyzed three days later (day 15 on the graph). (B) Percentage of Lyt-2<sup>+</sup> cells in the CD25<sup>+</sup> and CD25<sup>-</sup> fractions of resting T cells was determined on day 10 post-stimulation.

#### **Example 1: Vector constructions and retrovirus-producing cells**

##### Example 1A

The structures of the recombinant retrovirus vectors are shown in Figure 1. LMILy, MESV-MILy, MPSV-MILy, L587-MILy and LMSILy are derived from their MoMLV, MESV, MPSV, MoMLV/587 and MoMLV/SAR counterparts. The XhoI(blunt)-ClaI fragment spanning the tkNeo drug selection marker is exchanged for the BamHI(blunt)-ClaI IRES-Lyt-2 fragment. IRES-Lyt-2 consists of the internal ribosomal entry site (IRES) of the human encephalomyocarditis virus (EMCV) (Jang, S.K. et al. 1989 *J. Virol.* 63:1651-1660) linked to the Lyt-2  $\alpha'$  surface marker gene. Tagawa, M. et al. 1986 *Proc. Natl. Acad. Sci. USA* 83:3422-3426). The LMILy-2S is constructed by inserting the 800bp EcoRI-HindIII (blunt end) IFN- $\beta$  SAR fragment (Klehr, D. et al. 1991 *Biochemistry* 30:1264-1270) into the NheI

site in 3' LTR of the LXS<sub>N</sub> vector, and then the 3' LTR of LMILy is replaced by SAR-containing 3'LTR from the LXS<sub>N</sub>. LAMILY and LAMILY-2S contain a mutated RevM10 gene ( $\Delta$ M10) lacking the methionine initiation codon. Escaich, S. et al. 1995 *Hum. Gene Ther.* 6: 625-634. In addition, a 50 bp linker 5'-

GATCTGCTACGTGCATCGCTACCTGACTAGCTGACAGGCCATTCTGGCCT-3'

(SEQ.ID. NO.1) is inserted into the BglII site of the  $\Delta$ M10 gene (hatched box, Figure 1).

Vector LLYCD4N is constructed by inserting HindIII-ClaI Lyt-2 gene fragment into the EcoRI site of the LXS<sub>N</sub> (Miller, A.D. et al. 1989 *BioTechniques* 7: 980-990) and then the SV40-Neo fragment of LXS<sub>N</sub> is replaced by the human nerve growth factor receptor (NGFr) cDNA (1.5 kb BamHI-SacI fragment, Johnson, D. et al. 1986 *Cell* 47:545-554) under control of the human CD4 promoter (1.1 kb fragment, Salmon, P. et al. 1993 *Proc. Natl. Acad. Sci. USA* 90: 7739-7743.). Retroviral vector plasmid DNAs are transfected into BOSC-23 cells as described (Pear, W.S. et al. 1993 *Proc. Natl. Acad. Sci. USA* 90: 8392-8396.). Forty-eight hours post-transfection, BOSC-23 supernatants containing ecotropic retrovirus are used to inoculate PA317 cells (Miller, A.D. et al. 1986 *Molecular and Cellular Biology* 6: 2895-2902). Following transduction, Lyt-2-expressing PA317 cells are enriched using fluorescence activated cell sorter (FACS) to generate pools of producer cells. Retroviral vector supernatants are prepared as described in Forestell, S.P. et al. 1995 *Gene Therapy* 2: 723-730. Transduction efficiency of retroviral vector supernatants is determined on NIH3T3 cells. All producer cells are tested for the presence of replication competent retrovirus by S+L-assay on PG4 cells (Haapala, D.K. et al. 1985 *J. Virol.* 53:827-833.).

#### Example 1B

The MoMLV-based retroviral vector LMiLy (Fig. 1) encodes two genes from one bicistronic mRNA transcript (Fig. 6A): the RevM10 gene and the Lyt-2 surface marker (mouse CD8  $\alpha$ ' chain). Translation of the Lyt-2 protein is mediated by the IRES of the human EMCV and hence, linked to RevM10 protein expression. Double-staining of transduced CEMSS cells for RevM10 and Lyt-2 showed that expression of the two proteins is co-linear (Fig. 6B). Flow cytometric analysis of the easier detectable Lyt-2 surface antigen is subsequently used to estimate overall transgene expression. The 800bp IFNB-SAR fragment (as above) is inserted into the NheI site of the 3'LTR of the LMiLy generating the LMiLy2S vector. We have also

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generated MESV-based vectors because of their advantage over MoMLV for expression in hematopoietic cells. The MESV-MiLy2S and MESV-MiLy2S-F vectors are derived from the MESV-MiLy construct (Plavec I et al ,1997 *Gene Therapy* 7, 128-139.) (Fig. 1) . In LMiLy2S and MESV-MiLy2S, the SAR sequence is in the reverse, and in the MESV-MiLy2S-F in the forward orientation, as indicated by the arrows in Fig. 1. Forward and reverse refers to the orientation of the SAR element in its natural human IFN $\beta$  gene locus (Junker, U. et al 1995 *Gene Therapy* 2, 639-646). Following transduction, the 3'LTR SAR sequence is duplicated in the 5'LTR generating a double-copy type vector (Hantzopoulos, P. A. et al 1989 *Proc. Natl. Acad. Sci. USA* 86, 3519-3523.). Such double-copy vectors can be unstable ( Junker, U., et al 1995 *Gene Therapy* 2, 639-646). Clonal analyses of the LMiLy2S transduced CEMSS cells revealed instability of the vector. In about 30% of individual clonal CEMSS lines integrated proviruses did not contain SAR sequence (data not shown). Amphotropic producer cell lines were generated using ProPak-A packaging cells ( Rigg, J. R. et al. 1996 *Virology* 218, 290-295.) Since the vectors do not encode a drug resistance gene it is not possible to determine viral end-point titers. Instead, the ability of viral supernatants to transfer genes into NIH-3T3 cells is measured. Transduction efficiencies (Forestell, S. P., et al (1995) *Gene Therapy* 2, 723-730) of the retroviral stocks used were: LMiLy, 53%; MESV-MiLy, 81%; LMiLy2S, 21%; MESV-MiLy2S, 14%; and MESV-MiLy2S-F, 7%. All retroviral stocks were free of RCR.

#### Example 2: PCR analysis

For PCR analysis, cell lysates are prepared from 100,000 viable unfractionated or sorted cells. Cells are lysed in 200 $\mu$ l of a buffer containing 50 mM KCl, 10 mM Tris pH: 8.3, 2.5 MgCl<sub>2</sub>, 1% Tween 20, 1% NP40 and 100 mg/ml proteinase K at 56°C for 2 hours. After lysis, samples are incubated 30 minutes at 95°C to inactivate proteinase K. Primer used for amplification are: 5' LTR specific primers:-

Sar up2+: 5'-TCAATGGGTCTGTTTCTGAGCTCTA-3' (SEQ. ID. NO.2) and  
SDdn-: 5'-GGCGCATAAAATCAGTCATAGACAC-3' (SEQ. ID. NO.3);

3' LTR specific primers:-

Lyt up+: 5'-ACTTCGCCTGTGATATTTACATCTG-3' (SEQ. ID. NO.4) and



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LTR dn1-: 5'-TCTATCTGTTCTGACCTTGATCTG-3' (SEQ. ID. NO.5);

and endogenous  $\beta$ -globin gene specific primers:-

LA1: 5' ACACAACTGTGTTCACTAGC 3' (SEQ. ID. NO. 6) and

LA2: 5' CAACTTCATCCACGTTCAACC 3' (SEQ. ID. NO. 7).

Cells lysates are mixed with the PCR buffer (Perkin Elmer), dNTPs (Pharmacia) 200  $\mu$ M, 100 pmol of each primer and unit of Taq polymerase (Perkin Elmer). After denaturation (3 minutes at 95°C), the samples are submitted to 40 cycles of amplification: 1 minute 95°C, 2 minutes 59°C, 2 minutes 72°C, and 10 minutes elongation at 72°C in thermocycler (Perkin Elmer 4800). PCR products are analyzed by ethidium-bromide staining in 1.4% agarose gels.

### Example 3: Transduction of primary T-cells

Primary T-cells are isolated either from peripheral blood of healthy donors (PBL) or from thymus grafts of SCID-hu thymus/liver mice (thymocytes) (Plavec, I. et al. 1996 *Gene Therapy* 3, 717-724) and enriched for CD4+ cells by depleting CD8+ cells using anti-CD8 biotinylated Ab (Becton Dickinson) and streptavidin magnetic dynabeads (Dyna). This procedure yields a 90-95% pure CD4+ population. Cells are stimulated to divide in a TOC medium (RPMI supplemented with 1xMEM vitamin solution (GIBCO-BRL), insulin-transferrin-sodium selenite supplement (SIGMA) and 10% fetal bovine serum (Hyclone) with PHA (2  $\mu$ g/ml), IL-2 (40 U/ml) and allogeneic JY feeder cells (James, S.P. 1994 *In Current Protocols in Immunology*, vol. 1. R. Coico, editor. John Wiley & Sons, Inc., New York. and Plavec, I.. 1997 *Gene Therapy* 7, 128-139) for 3-4 days. Retroviral vector transduction is performed by centrifugation of  $5 \times 10^5$  cells with 1 ml of supernatant from retroviral producer cells supplemented with 8  $\mu$ g/ml polybrene for 3 hours at 2000 xg and 34°C. This procedure is performed on two consecutive days. The transduced cells are generally enriched by two rounds of positive selection using anti-Lyt-2 biotinylated Ab (PharMingen) and streptavidin magnetic dynabeads (Dyna) or using fluorescence activated cell sorter (FACS). For analysis of retroviral vector gene expression, cells are stimulated with PHA and feeders as described above and at various time points post-stimulation aliquots of cells are double stained with anti-Lyt-2 R-PE (PharMingen) and anti-CD25 FITC (Beckton Dickinson) antibodies and

analyzed on a FACScan (Beckton Dickinson). Expression of NGFr is analyzed using FITC-conjugated anti-NGFr antibody (MoAb 20.4, ATCC#HB8737).

### Example 3A

**The effect of the SAR sequence on transgene expression is most pronounced in the CD25<sup>-</sup> compartment of resting T cells.**

Cellular Lyt-2 expression levels (mean fluorescence intensity) of LMiLy- and LMiLy2S-transduced populations are analysed (Table 2). The CD25<sup>-</sup> gate is defined using control isotype antibodies (data not shown). On average, there are  $5.7 \pm 3.4$  fold more Lyt-2<sup>+</sup> cells in the CD25<sup>-</sup> fraction of the LMiLy2S than of the LMiLy-transduced populations (Table 2). In contrast, there are only  $1.7 \pm 0.5$  fold more Lyt-2<sup>+</sup> LMiLy2S- than the LMiLy-transduced cells in the CD25<sup>+</sup> fraction (Table 2). The mean fluorescence intensity of the Lyt-2 staining, which is taken as an indirect measure for transgene expression level, is only slightly increased (1.6 fold) in the LMiLy2S compared to the LMiLy-transduced cells and there was no detectable difference between the CD25<sup>-</sup> and CD25<sup>+</sup> cell fractions (Table 2).

Two populations of resting LMiLy2S-transduced T cells are observed: 30-40% of the cells are Lyt-2<sup>+</sup> and the rest are Lyt-2<sup>-</sup> (Fig. 8F.). To further characterise those populations, the Lyt-2<sup>+</sup> and the Lyt-2<sup>-</sup> cells are separated using FACS and analysed by semiquantitative PCR for the presence of the SAR sequence in the proviral DNA (Fig. 3B). The Lyt-2<sup>+</sup> cells show strong SAR-specific PCR signals indicating SAR sequence copies present both in the 5' and the 3' LTR. In contrast, the Lyt-2<sup>-</sup> cells yield faint SAR-specific signals implying that a significant portion of integrated retroviral proviruses has lost the SAR sequence, in agreement with our observations about the instability of the LMiLy2S vector. Lyt-2<sup>-</sup> cells contain however, transcriptionally competent proviruses as demonstrated by expression of the Lyt-2 marker upon re-stimulation of these cells (data not shown).

Table 2. Expression of the Lyt-2 surface marker in the CD25<sup>-</sup> and CD25<sup>+</sup> subpopulations of resting primary T cells transduced with the LMiLy and LMiLy2S vectors.

Tissue*		Percent Lyt-2 <sup>+</sup> cells						Relative transgene expression (Lyt-2 mean fluorescence intensity)					
		CD25 <sup>-</sup> fraction			CD25 <sup>+</sup> fraction			CD25 <sup>-</sup> Lyt-2 <sup>+</sup> fraction			CD25 <sup>+</sup> Lyt-2 <sup>+</sup> fraction		
		LMiLy	LMiLy2S	Ratio $\frac{\text{LMiLy2S}}{\text{LMiLy}}$	LMiLy	LMiLy2S	Ratio $\frac{\text{LMiLy2S}}{\text{LMiLy}}$	LMiLy	LMiLy2S	Ratio $\frac{\text{LMiLy2S}}{\text{LMiLy}}$	LMiLy	LMiLy2S	Ratio $\frac{\text{LMiLy2S}}{\text{LMiLy}}$
1	3	19	6.3	12	20	1.7		25	41	1.6	32	48	1.5
2	1	11	11	6	15	2.5		23	35	1.5	26	39	1.5
3	7	20	2.9	26	28	1.1		27	46	1.7	44	76	1.7
4	9	22	2.4	26	33	1.3		23	41	1.8	32	54	1.7
Average		5.7±3.4			1.7±0.5			1.65±0.1			1.6±0.1		

Samples are analysed 10-12 days post-stimulation with PHA, IL-2 and allogenic feeder cells. Gates for the CD25<sup>-</sup> fractions are set using control isotype antibodies. Quantitative analysis of the Lyt-2 staining was performed when approximately 50% of the total cells fell into the CD25<sup>-</sup> gate (see Figure 8, panel D). \* Tissues 1 and 4 are thymocytes, and 2 and 3 are PBLs.

**Example 3B**

**The SAR sequence enhances transgene expression in an orientation-dependent manner.** The SAR sequence is able to rescue expression of the MESV-based retroviral vector MESV-MiLy (Fig. 1) which is also down-regulated in resting primary T cells (Rigg, J. R. 1996 *Virology* 218, 290-295). Kinetic analysis of Lyt-2 expression in transduced T cell cultures demonstrates that the MESV-MiLy2S vector behaves similarly to the LMiLy2S vector (Fig. 9A). Compared to MESV-LMiLy, the Lyt-2 transgene is better expressed in the MESV-MiLy2S transduced CD25<sup>+</sup> resting T cell fraction. Furthermore, the cell number in the Lyt-2<sup>+</sup>CD25<sup>+</sup> fraction is comparable to the LMiLy2S vector (Fig. 9B). The positive effect is observed only when the SAR sequence is present in the reverse orientation (compare MESV-MiLy2S and MESV-MiLy2S-F vectors, Fig. 9). Interestingly, when the SAR element is in the forward orientation (vector MESV-MiLy2S-F) transgene expression is lower than even with the parental MESV-MiLy vector. Similarly, lower transgene expression is also seen with the LMiLy2S-F vector which carries the SAR sequence in the forward orientation (data not shown).

**Example 4: HIV infection of primary T-cells**

On day 4-5 following stimulation, cells are washed and resuspended in TOC medium containing IL-2 alone.  $2-3 \times 10^4$  cells in 75 $\mu$ l volume are mixed with 75 $\mu$ l of an undiluted JR-CSF HIV-1 virus stock ( $10^4-10^5$  TCID<sub>50</sub>/ml) and then plated in triplicate in the wells of round-bottom 96-well plates. Cells are cultured overnight and on the following day 125 $\mu$ l of medium is removed and replaced with 135 $\mu$ l of fresh TOC + IL-2. In this way cell supernatants are harvested on days 3, 5, 7, and 9 post inoculation. Where indicated, on day three, 135  $\mu$ l TOC/IL-2 containing  $2.5 \times 10^5$  feeder cells/ml is added to the cells. HIV-1 p24 antigen concentration in the culture supernatants is determined using an ELISA kit (Dupont-NEN).

**Example 5: Expression of standard retroviral vectors in non-stimulated T-cells.**

We have previously observed that the expression of the MoMLV-based retroviral vectors is down regulated in non-stimulated primary human T-cells. We were interested in identifying retroviral vectors which would allow expression in non-stimulated cells. We tested vectors

based on myeloproliferative sarcoma virus (MPSV), murine embryonic stem cell virus (MESV), and a MoMLV-based vector which contains a primer binding site from the dl587-rev virus (Figure 1, vectors MESV-MILy, MPSV-MILy and L/587-MILy). All these vectors encode Lyl-2 surface marker which allows easy and quantitative analysis of expression (Figure 1). Primary CD4+ T-cells are stimulated in vitro with PHA, IL-2 and allogeneic feeder cells for 3-4 days and then transduced with retroviral vectors by centrifugation (Bahnon, A.B., et al. (1995) *J. Virol. Methods* 54:131-143). Following this protocol, we detect 4-8% Lyl-2 positive cells and after expansion in vitro, the Lyl-2 positive cells are further enriched to 80-90 % purity using immunomagnetic beads. These cells are then stimulated in a medium containing PHA and feeders. The CD25 surface protein (low affinity IL2 receptor) is used as a marker for the T cell activation status. Three to five days post stimulation, CD25 expression is at a maximum with greater than 95% CD25<sup>+</sup> cells (Figure 8A). By days 11-14, cells ceased to proliferate and the CD25 marker was down-regulated (>50% CD25<sup>-</sup> cells ) reflecting the mitotically resting state of these primary T cells (Figure 8D). Expression of retroviral vectors in stimulated and non-stimulated cultures is determined by staining cells for Lyl2 expression with the anti-Lyl2 antibodies. Results are shown in Table 1A. Expression of Lyl-2 in LMILy, MESV-MILy, MPSV-MILy and L/587-MILy transduced cells is down-regulated as the cells become non-stimulated. On day 11 post stimulation, approximately 50% of cells are CD25<sup>-</sup> and 50% are CD25<sup>+</sup>. The majority of the Lyl-2+ cells are present in CD25<sup>+</sup> population and very few in the CD25<sup>-</sup> population .

We reasoned that CD25<sup>-</sup> cells lack transcription factors required for retroviral vector LTR expression. To test this hypothesis a vector is prepared in which expression of a marker gene (in this case it is the human NGF receptor, supra) is driven by the 1.1kb human CD4 promoter (supra) (Figure 1, vector LLYCD4N). CD4 molecule is expressed normally at high levels in non-stimulated T-cells. Expression of NGFr from the CD4 promoter in the retrovirally transduced cells, however, is down-regulated in CD25<sup>-</sup> cells and this down-regulation appears to go in parallel with the down-regulation of the expression of the MoMLV LTR promoter, indicating that the down-regulation is characteristic of the retroviral vector, not the specific promoter used.

**Table 1A.** *Expression of retroviral vectors in CD4+ T-cells on day 11 post stimulation.*

Vector	% expressing cells	Mean fluorescence
LMILy	6	16
LΔMILy	8	16
MESV-MILy	7	18
MPSV-MILy	2	16
L/587-MILy	7	16
LLyCD4N	9	19
LMSILy	17	19
LMILy2S	23	27
LΔMILy2S	30	22

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Table 1B. Expression of the Lyt-2 surface marker in activated and resting primary T cells transduced with the LMiLy and LMiLy2S vectors.

Tissue*	Activated			Resting		
	Percent Lyt-2 <sup>+</sup> cells			Percent Lyt-2 <sup>+</sup> cells		
	LMiLy	LMiLy2S	Ratio $\frac{\text{LMiLy2S}}{\text{LMiLy}}$	LMiLy	LMiLy2S	Ratio $\frac{\text{LMiLy2S}}{\text{LMiLy}}$
1	91	96	1.05	15	39	2.6
2	65	64	0.98	7	26	3.7
3	73	86	1.18	33	48	1.5
4	95	96	1.01	35	55	1.6
Average			1.06±0.08			2.4±0.9

Samples are analyzed on day 3 (Activated) and day 10-12 (Resting) post-stimulation with PHA, IL-2 and allogeneic feeder cells.

Gates for the Lyt-2<sup>+</sup> cells are set using untransduced T cells as control (see Figure 8, panels A and D).

\* Tissues 1 and 4 are thymocytes, and 2 and 3 are PBLs.

**Example 6: Vectors containing scaffold attachment region (SAR) maintain expression in non-stimulated T-cells.**

**We analysed Lyt-2 transgene expression in activated (day 3 post stimulation ) and resting cells (day 11 post stimulation).**

Results obtained with one representative tissue are shown in Figure 8. There is no marked difference in the percentage of the Lyt-2<sup>+</sup> cells between the LMiLy (91%) and the LMiLy2S (96%) vectors in activated T cells (Fig. 8, panels B and C). In resting cells, overall Lyt-2 expression was lower (Fig. 8, compare panels B and C to E and F), and the loss of transgene expression correlates with the decrease of the CD25 marker. However, we observe a significant difference in Lyt-2 expression between the LMiLy and the LMiLy2S vectors. Fifteen percent of the LMiLy transduced cells are Lyt-2 positive compared to 39% for the LMiLy2S vector (Fig. 8, panels E and F). Upon re-stimulation, both LMiLy- and LMiLy2S-transduced cells express comparable high levels of the Lyt-2 marker (87% and 95%, respectively) demonstrating that the observed loss of expression is not caused by loss of integrated vector (data not shown and Figure 9A). Similar expression patterns are observed irrespective of the source of primary T cells. The data obtained with four independent tissues (two PBLs and two thymocytes) is summarized in Table 1B. Although the absolute percentage of Lyt-2<sup>+</sup> resting T cells varies considerably from tissue to tissue, the LMiLy2S vector consistently yields higher values (on average  $2.4 \pm 0.9$  fold more Lyt-2<sup>+</sup> cells) than the LMiLy vector (Table 1B).

**Example 7: Inhibition of HIV replication**

To test whether improved expression would result in more effective RevM10-mediated inhibition of HIV-1 replication, primary CD4<sup>+</sup> T cells transduced with the LMiLy, LMSiLy LMiLy2S vectors are inoculated with the HIV-1 JR-CSF strain and viral replication is monitored over a period of 9 days (Figure 4). Cells transduced with the LMiLy vector which does not produce RevM10 protein (supra) are used as a negative control. Cells are inoculated with HIV-1 JR-CSF on day 5 post stimulation with PHA, IL-2 and feeder cells



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("Day 5" samples). To make a comparison between stimulated (activated) and non-stimulated (non-activated) cells, on day three post inoculation with HIV, half of the cultures are fed fresh PHA and feeder cells to maintain stimulated phenotype of T-cells. As shown in Fig. 4B, the LMiLy2S vector is not only more potent in inhibiting HIV replication in activated cells but it maintains its efficacy even in resting cells whereas the LMiLy vector lost its anti-viral effect (Fig. 4A). The anti-viral effect of the LMiLy2S vector was solely due to RevM10 protein expression since a control SAR vector (L $\Delta$ MiLy2S) which does not encode RevM10 protein had no effect on HIV-1 replication (data not shown). As expected, there was no difference in anti-viral efficacy between the two vectors in HIV-1 HXB-3 infected CEMSS cell populations (data not shown).

**Example 8: Differential expression in SAR-transduced primary and cultured cells**

**RNA Analysis:** Total Cellular RNA extracted from CEM SS cells (human CD4+ T cells) and thymocytes using Rnazol B (Ambion, Austin TX) is analyzed by RNase protection using the Ambion RPA II kit. RNA probes are synthesized using plasmids derived from pBluescriptKS+ (Stratagene) by in vitro transcription with either T3 or T7 polymerase using <sup>32</sup>P-UTP according to the Bluescript Instruction Manual. The RNA probes corresponding to 188bp HindIII-BamHI fragment internal to the Rev gene and 100 bp PstI-Sall PCR fragment spanning the third exon of the human  $\beta$ -actin gene from positions 1450 to 1550 (GenBank file HUMACTB-CYT-A). The assay is performed by hybridizing  $\approx$  1 $\mu$ g total cellular RNA and 9  $\mu$ g yeast carrier RNA with 1-2x10<sup>5</sup> cpm of each probe. Protected fragments are separated on a 5% polyacrylamide-7M urea denaturing gel and visualized by autoradiography. Radioactivity in protected fragments is quantitated using a Phosphorimager (Molecular Dynamics). Relative expression of RevM10 is estimated by using the actin-specific signals as an internal reference to correct for differences in the amount of RNA loaded in different lanes.

We have found that SAR enhances expression of retroviral vectors in primary T-cells but not in cultured cells (specifically, the CEM SS T-cell line or PA317-mouse fibroblast cell line). CEM SS cells transduced with the LMiLy, LMSiLy and LMiLy2S vectors show patterns of Lyt-2 staining similar to that observed in stimulated or active thymocytes (data not

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shown. As is shown in Figure 6 the presence of the SAR element has no effect on transgene expression levels in the established human T cell line nor in the murine cells.

To further analyze the expression of SAR-containing vectors at the molecular level we have isolated total cellular RNA from transduced CEM SS cells and both stimulated and non-stimulated thymocytes. Steady-state level of vector-specific RNA was determined by semiquantitative RNase protection assay. Values obtained in the assay are shown in Figure 5. Values obtained in CEM SS cells and thymocytes are separately normalized relative to the appropriate LMILy vector RNA. RNA analysis corroborates the results obtained by Lyt-2 staining in primary thymocytes. SAR stimulates the expression of retroviral vectors up to three-fold in both stimulated and non-stimulated thymocytes and again the double SAR configuration is more effective than the single SAR. Interestingly, SAR has no effect on vector RNA expression in transduced CEM SS cells (Figure 5) underscoring the difference between primary and immortalized T-cells.

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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

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(ii) TITLE OF INVENTION: Organic Compounds

(iii) NUMBER OF SEQUENCES: 7

## (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GATCTGCTAC GTGCATCGCT ACCTGACTAG CTGACAGGCC ATTCTGGCCT

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## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TCAATGGGTC TGTTCCTGAG CTCTA

25

## (2) INFORMATION FOR SEQ ID NO: 3:

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- (i) SEQUENCE CHARACTERISTICS:
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  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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25

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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25

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
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  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- 25 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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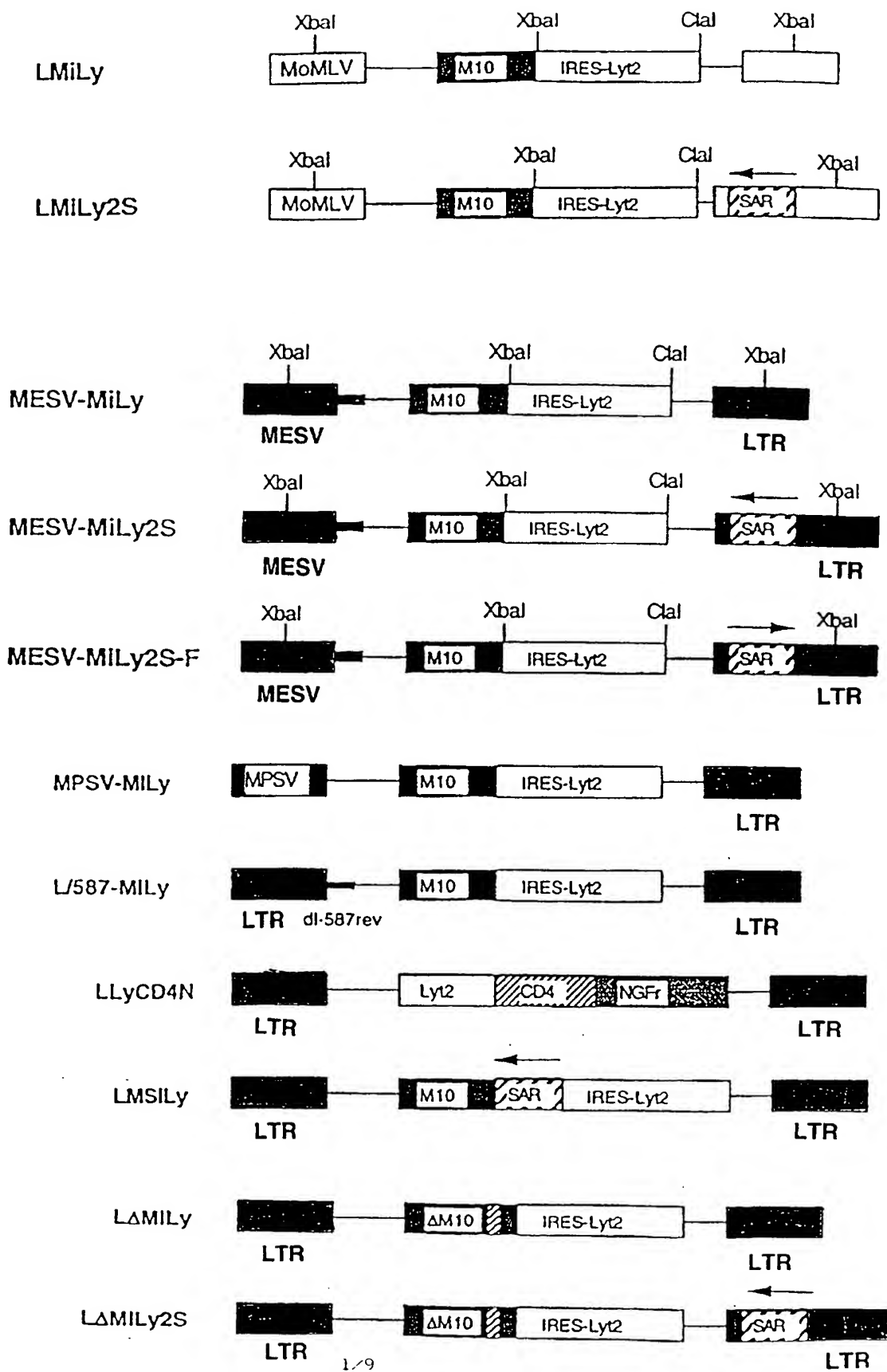
20

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## CLAIMS

1. Use of a DNA scaffold or matrix attachment region (SAR) to increase gene expression in retrovirally transduced eukaryotic non-immortal resting cells.
2. A method of modifying expression of a heterologous gene in a retrovirally transduced eukaryotic cell comprising transducing a non-immortal cell with a retrovirus comprising (i) at least one heterologous gene operatively linked to an expression control sequence and (ii) at least one SAR.
3. A method of increasing expression of a heterologous gene in a retrovirally transduced eukaryotic resting cell comprising transducing a non-immortal eukaryotic resting cell with a retrovirus comprising (i) at least one heterologous gene operatively linked to an expression control sequence and (ii) at least one SAR, the SAR being in the reverse direction.
4. A method of down regulating expression of a heterologous gene in a retrovirally transduced eukaryotic resting cell comprising transducing a non-immortal cell with a retrovirus comprising (i) at least one heterologous gene operatively linked to an expression control sequence and (ii) at least one SAR, the SAR being in the forward direction.
5. A retroviral vector comprising genetic material corresponding to (a) at least one SAR, and (b) at least one heterologous gene operatively linked to an expression control sequence, the heterologous gene (or at least one of the heterologous genes if there is more than one heterologous gene) being rev-M10 and the SAR or at least one SAR is derived from, obtainable from or corresponds to the 5' SAR of the human interferon- $\beta$  gene.
6. A cellular composition comprising non-immortal human cells transduced with a retroviral vector as claimed in claim 5.

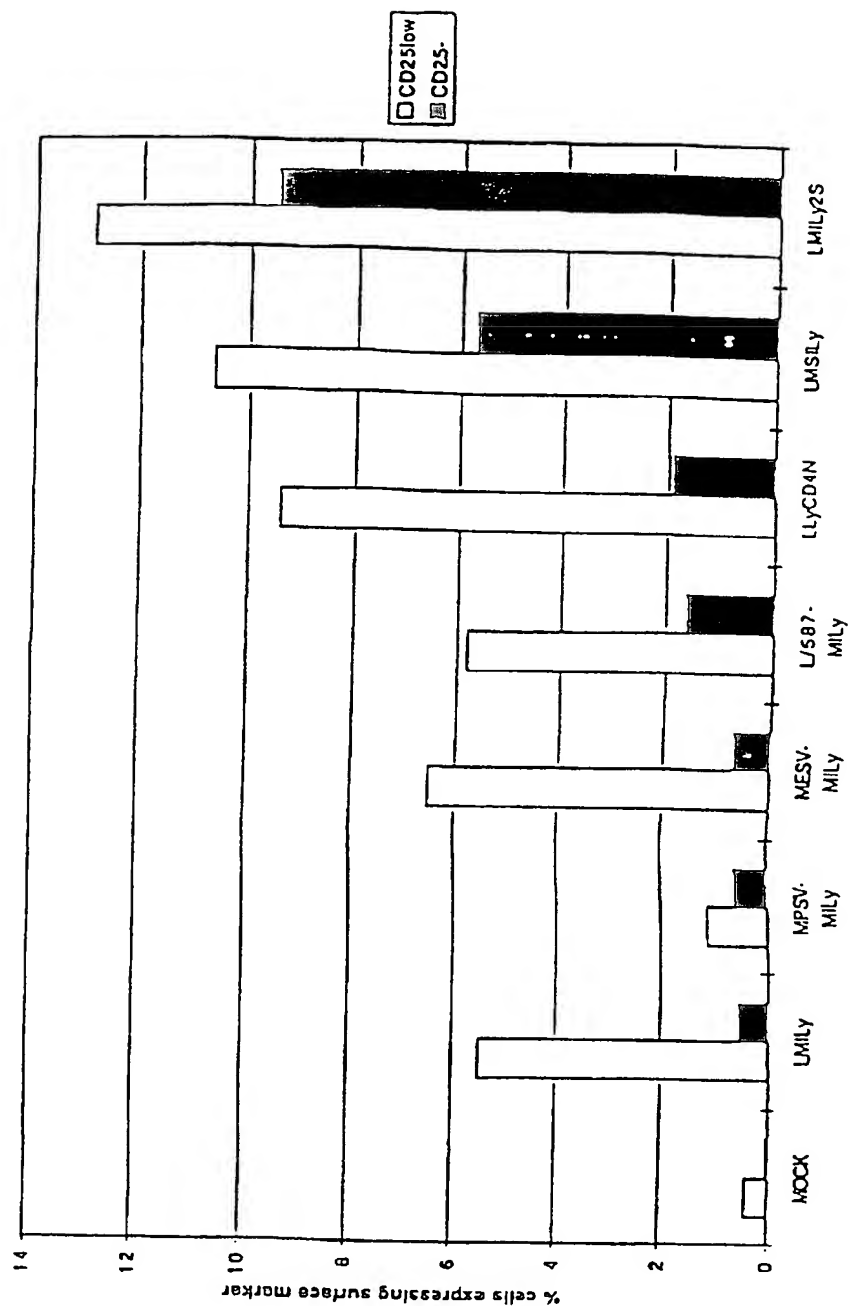
7. A cellular composition according to claim 6 wherein the cells are hematopoietic cells.
8. A cellular composition according to claim 7 wherein the cells are T cells.
9. A method of gene therapy for a patient in need thereof, comprising introducing into said patient, a cellular composition according to any one of claims 6, 7 or 8.
10. The method according to claim 9 comprising the steps of removing hematopoietic cells from said patient, transducing said cells with a vector according to claim 5, and reintroducing the transduced cells into the patient.
11. A method of treating a patient suffering from HIV infection, e.g., HIV-1 infection, comprising removing and isolating hematopoietic cells (e.g., hematopoietic stem cells, peripheral blood lymphocytes, CD4+ cells or T cells derived from hematopoietic stem cells) from said patient; transducing the cells with a gene for an anti-retroviral protein (e.g., rev-M10) and a SAR (e.g., a SAR derived or obtainable from the 5' SAR of human IFN- $\beta$ ), and reintroducing the cells into the patient.
12. All novel products, processes, and utilities substantially as described herein, especially with reference to the examples.

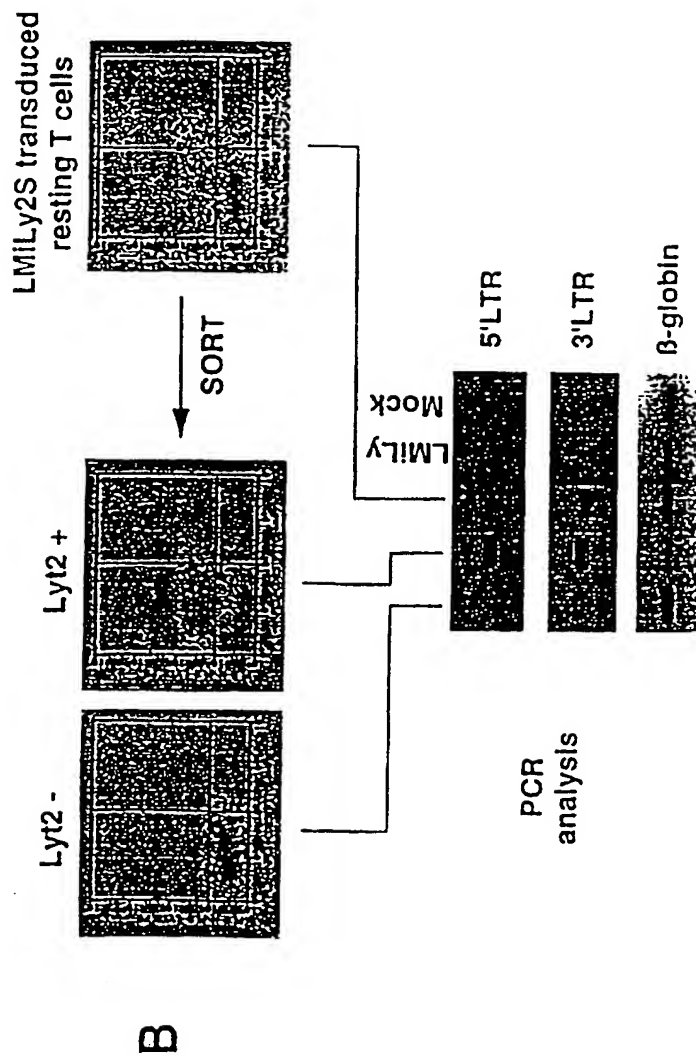


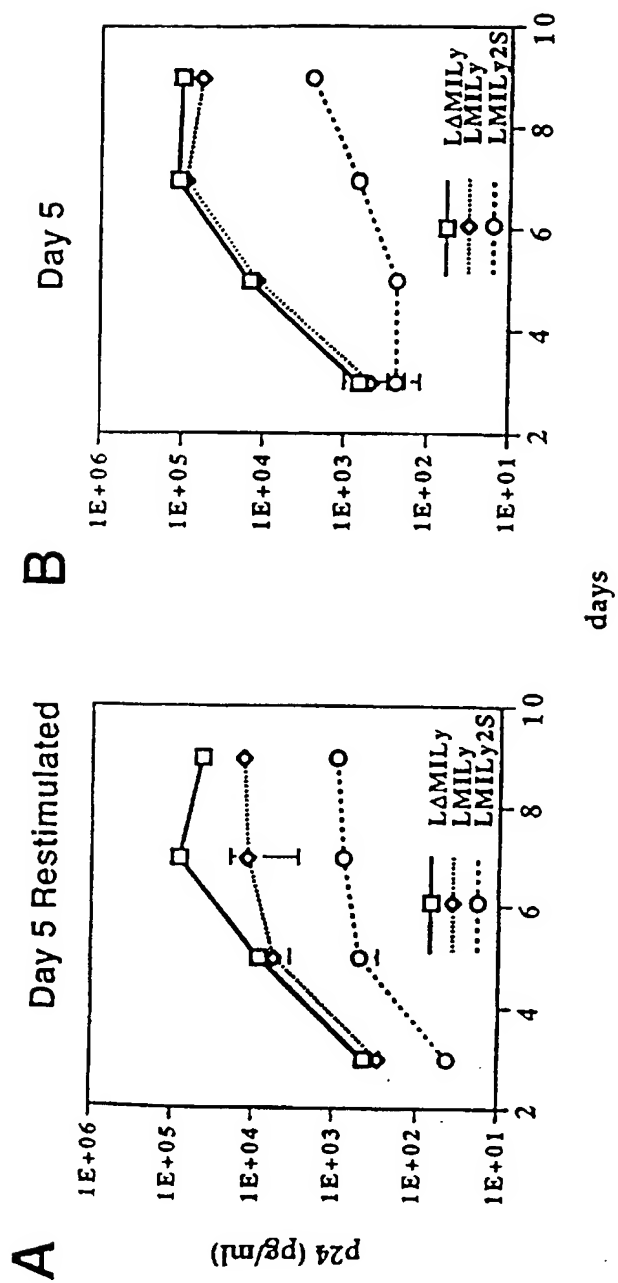


Ly12 over CD25 neg Chart 4

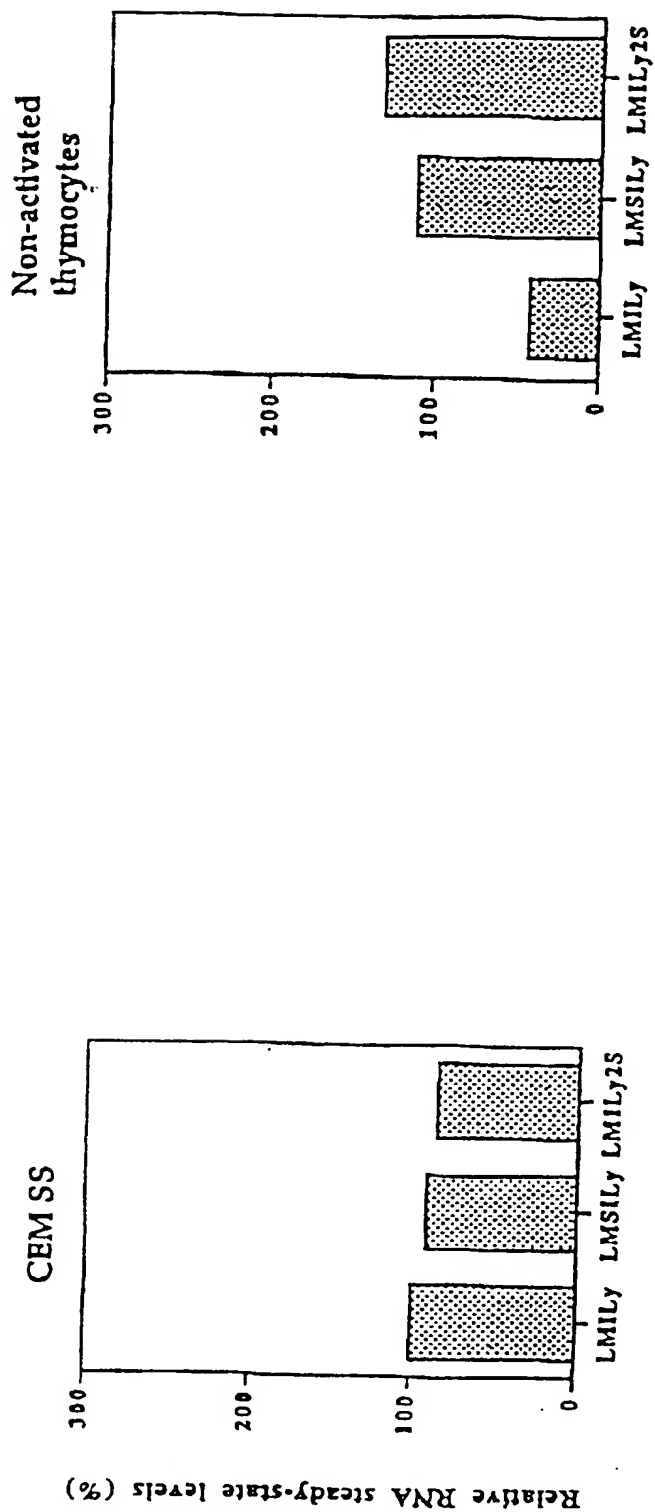
Expression of retroviral vectors in CD25low and CD25- cell population on day 11 post stimulation



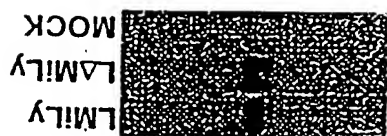




# Effect of SAR on expression of retroviral vector RNA in primary T-cells and CEM SS T-cell line

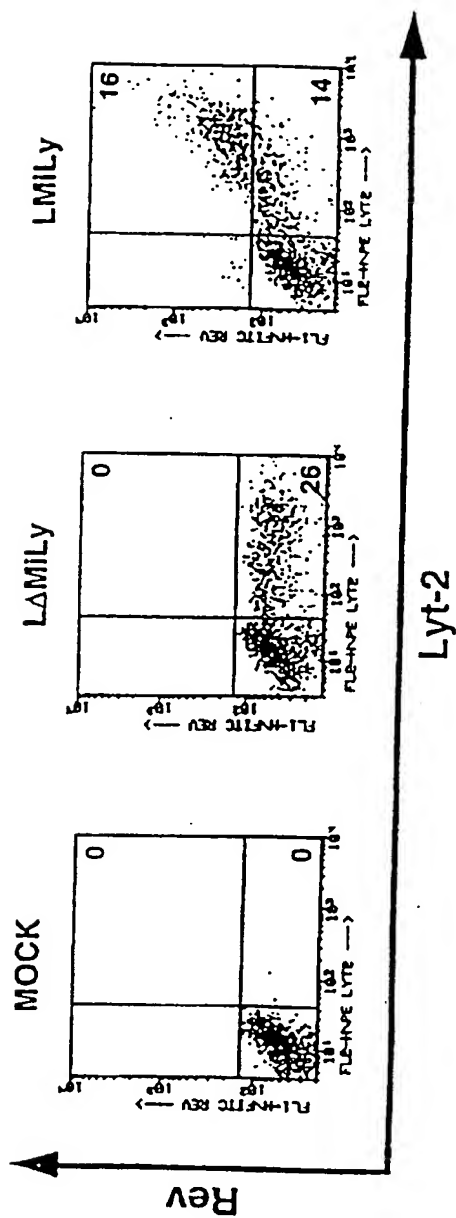


A



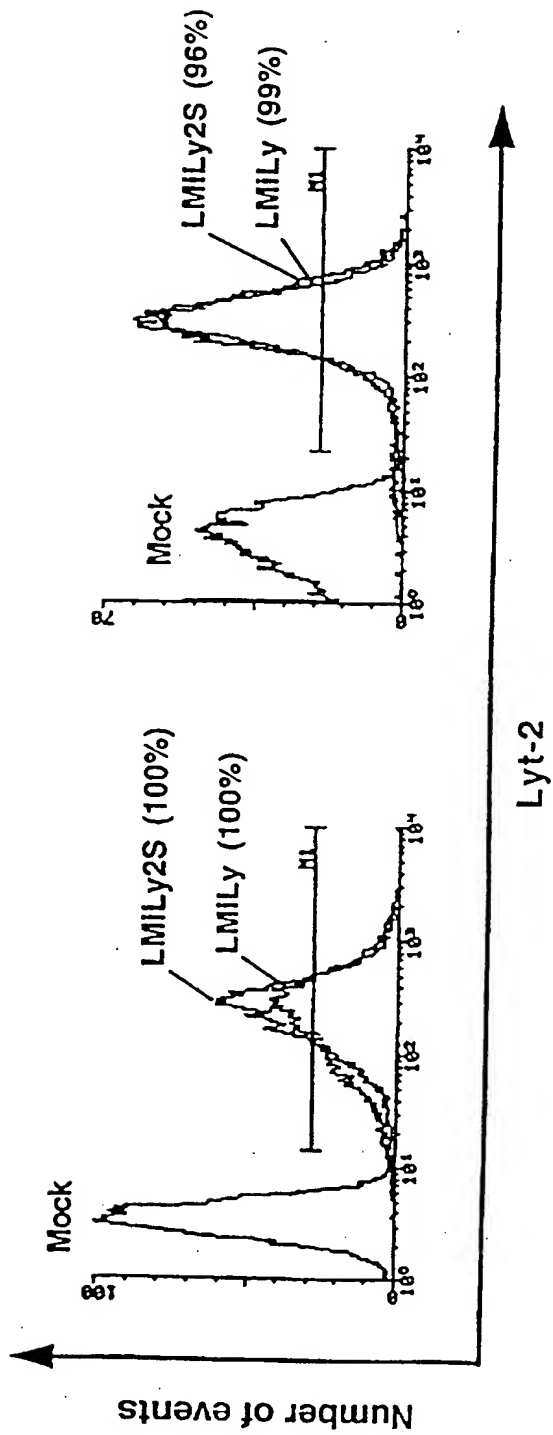
RevM10 RNA →

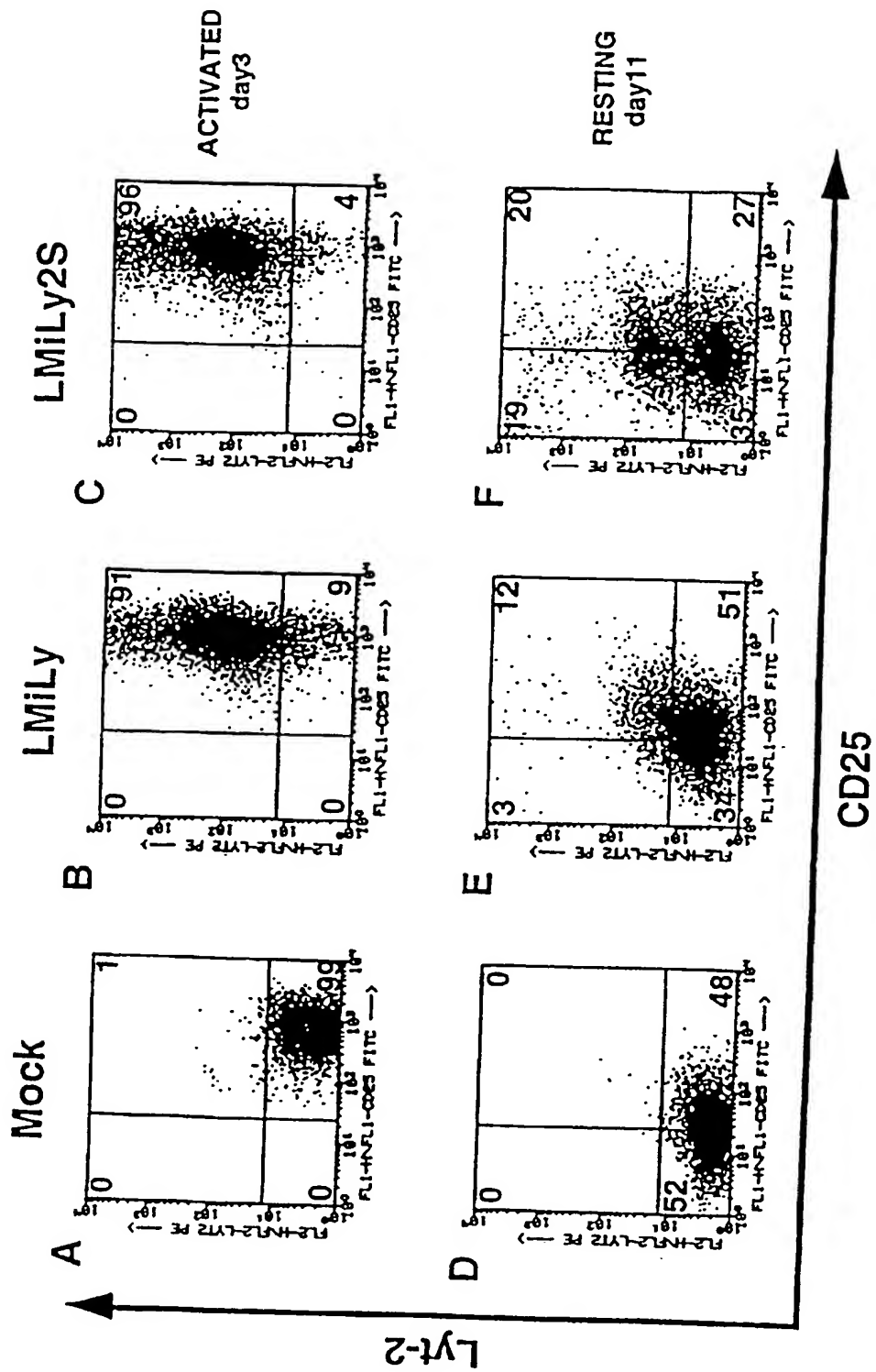
B



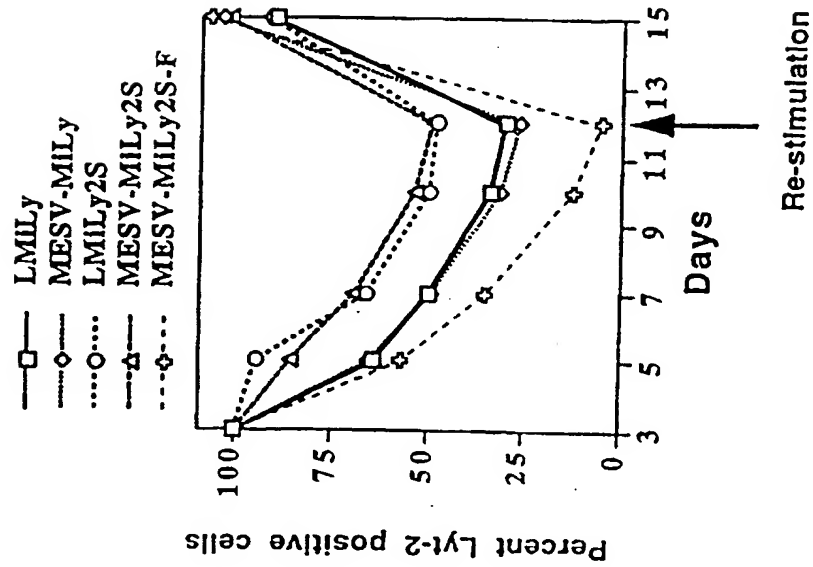
CEMISS

PA317

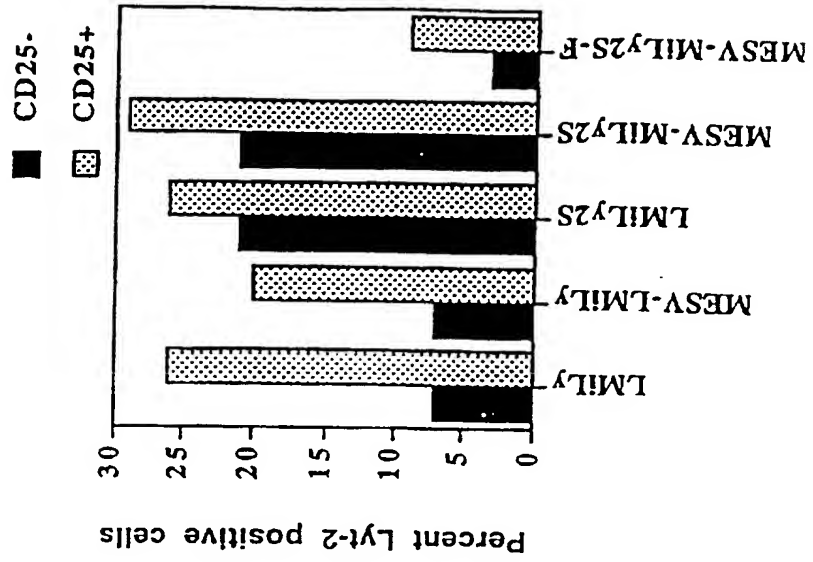




A



B





# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/EP 97/02972

A. CLASSIFICATION OF SUBJECT MATTER  
IPC 6 C12N15/49 C12N15/85 C12N15/86 C12N5/10 C07K14/16  
A61K48/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	D. BEVEC ET AL.: "Inhibition of human immunodeficiency virus type 1 replication in human T cells by retroviral-mediated gene transfer of a dominant-negative Rev trans-activator" PROC. NATL.ACAD SCI., vol. 89, October 1992, NATL. ACAD SCI., WASHINGTON, DC, US;, pages 9870-9874, XP002038935 see the whole document ---	5-11
A	WO 90 14427 A (SANDOZ LTD ;UNIV DUKE (US)) 29 November 1990 cited in the application see the whole document --- -/-	5-11

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

\* Special categories of cited documents:

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
- \*E\* earlier document but published on or after the international filing date
- \*L\* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

- \*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- \*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- \*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- \*A\* document member of the same patent family

Date of the actual completion of the international search

11 September 1997

Date of mailing of the international search report

16.09.97

Name and mailing address of the ISA

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Fax (+ 31-70) 340-3016

Authorized officer

Hornig, H

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 97/02972

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	ESCAICH S ET AL: "REVM10-MEDIATED INHIBITION OF HIV-1 REPLICATION IN CHRONICALLY INFECTED T CELLS" HUMAN GENE THERAPY, vol. 6, May 1995, pages 625-634, XP000653174 cited in the application see the whole document	5-11
A	--- D. KLEHR ET AL.: "Scaffold-attached regions from the human interferon beta domain can be used to enhance the stable expression of genes under the control of various promoters" BIOCHEMISTRY, vol. 30, no. 5, 5 February 1991, AM. CHEM. SOC., WASHINGTON, DC, US, pages 1264-1270, XP002038936 cited in the application see the whole document	1-12
A	--- L. PHI-VAN ET AL.: "The chicken lysozyme 5' matrix attachment region increases transcription from a heterologous promoter in heterologous cells and dampens position effects on the expression of transfected genes" MOL. CELL. BIOL., vol. 10, no. 5, May 1990, ASM WASHINGTON, DC, US, pages 2302-2307, XP002038937 see the whole document	1-12
A	--- WO 95 20653 A (AGRONOMIQUE INST NAT RECH) 3 August 1995 see page 7, line 3 - page 8, line 36	1-12
A	--- R.J. RIGG ET AL.: "A novel human amphotrophic packaging cell line: High titer, complement resistance, and improved safety" VIROLOGY, vol. 218, no. 1, 1 April 1996, ACADEMIC PRESS, INC., NEW YORK, US, pages 290-295, XP000570621 see the whole document	1-12
P,X	--- WO 96 19573 A (CANGENE CORP ; DELCUVE GENEVIEVE (CA)) 27 June 1996 see page 17, line 23 - line 27 see page 25, line 3 - line 12 see page 25, line 18 - page 26, line 4 --- -/--	1-3,12

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 97/02972

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,A	1. PLAVEC ET AL.: "Sustained retroviral gene marking and expression in lymphoid cells derived from transduced hematopoietic progenitor cells" GENE THERAPY, vol. 3, no. 8, August 1996, MACMILLAN PRESS, UK, pages 717-724, XP002038938 cited in the application see the whole document ---	1-12
P,A	1. PLAVEC ET AL.: "High transdominant RevM10 protein levels are required to inhibit HIV-1 replication in cell lines and primary T cells: implication for gene therapy of AIDS" GENE THERAPY, vol. 4, no. 2, February 1997, MACMILLAN PRESS, UK, pages 128-139, XP002038939 cited in the application see the whole document -----	1-12

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/EP 97/02972

**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
Remark: Although claim(s) 9 - 11  
is(are) directed to a method of treatment of the human/animal  
body, the search has been carried out and based on the alleged  
effects of the compound/composition.
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such  
an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all  
searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment  
of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report  
covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is  
restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 97/02972

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9014427 A	29-11-90	AU 648256 B	21-04-94
		AU 5738890 A	18-12-90
		AU 678478 B	29-05-97
		AU 6757394 A	17-11-94
		CA 2032158 A	26-11-90
		EP 0406557 A	09-01-91
		HU 9500249 A	28-11-95
		JP 4500009 T	09-01-92
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WO 9520653 A	03-08-95	FR 2715665 A	04-08-95
		AU 1581995 A	15-08-95
		CA 2181264 A	03-08-95
		EP 0742819 A	20-11-96
		ZA 9500659 A	07-02-96
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WO 9619573 A	27-06-96	AU 4169296 A	10-07-96
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